

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model					
Result No.	Score	Query Match	Length	DB	Description
1	406	9.9	2436	16	PATNTIA
2	355	7.6	5502	3	AB023139
3	366	7.5	6291	9	AB035266
4	270	5.6	153169	2	AP031002
5	270	5.6	552	2	AP001462
6	270	5.6	552	2	AC030475
7	270	5.6	552	2	AC044700
8	270	5.6	552	2	AB035356
9	270	5.6	552	2	AB011150
10	270	5.6	552	2	AC09260
11	270	5.6	552	2	AX351021
12	200	6.6	414	9	AB011150
13	189	8.8	411	9	AC018286
14	198	8.8	411	9	AC035356
15	193	8.8	400	4	ECVNEURXIA
16	190	8.8	394	9	AC007462
17	189	8.8	390	10	RATNTIA
18	161	9.9	324	4	GGAN00473
19	132	4.4	274	9	AC124002
20	125	4.2	259	2	AC009260
21	124	4.2	257	2	AC009260
22	124	4.2	256	2	AC101069
23	120	4.2	248	2	AC107855
24	125	4.2	247	2	AC123211
25	99	20.5	99072	2	AC130096
26	79	26.2	179525	2	AC094760
27	77	24.8	195172	2	AC101311
28	63	23.2	121	2	AC111255
29	58	22.0	98902	2	AC128547
30	50	10.4	125020	9	AP429315
31	46	9.5	115666	2	AC105744
32	42	9.8	41611	2	AC017806
33	42	9.8	164193	3	AC006494
34	42	9.8	179254	3	AC009196
35	42	9.8	223915	3	AE003739
36	42	9.8	7219	3	DROCRPA
37	42	9.8	156905	2	AC020006
38	42	9.7	199616	3	AC009204
39	42	9.7	304443	2	AE003747
40	41	9.6	162712	2	AC015677
41	41	9.6	164343	9	AP001099
42	41	8.5	157383	2	AC112534
43	40	8.4	909	1	AB085185
44	40	8.3	15098	1	AE004204
45	40	8.3	15169	1	PSNARFL
ALIGNMENTS					
RESULT 1					
RATNTIA					
LOCUS					
PATNTIA					
DEFINITION Rattus norvegicus neurokinin-1-like (pre-pro-) (alternatively spliced) mRNAs, complete cds.					
ACCESSION M96376					
VERSION M96376.1					
KEYWORDS synaptic protein; laminin; neurexin III-alpha;					
SOURCE Rattus norvegicus (strain Sprague Dawley) library; Graragene;					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
38:	em_sy:	*			
39:	em_htgc_hum:	*			
40:	em_htgo_mus:	*			
41:	em_htgo_other:	*			

RESULT 4
AP001092/c
LOCUS AF001092 153169 bp ERA linear HT3 23 JAN 2001
DEFINITION Homo sapiens chromosome 11 clone RP11-727K3 map 11q13, WORKING
ACCESSION AP001092
VERSION AP001092 4 GI:12226055
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone RP11-727K3
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
REFERENCE 1 (bases 1 to 153169)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hori-Suzuki,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens 153,169 genomic DNA of 11q13
JOURNAL Published Only in DataBase (2000)
REFERENCE 2 (bases 1 to 153169)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Saeg, P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
SUBMITTED (25-JAN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehirc-cho, Tsukumi-ki, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsr.riken.go.jp, http://hgr.gsc.riken.go.jp/),
tel:81-45-503-9111, Fax:81-45-503-9170
ON JAN 23, 2001 this sequence version replaced gi:8217802
COMMENT ----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgr.gsc.riken.go.jp/
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-727K3
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 245474 bases at least Q40
Consensus quality: 148742 bases at least Q20
Consensus quality: 153169 bases at least Q20
Insert size: 150869; sum-of-contigs
Quality coverage: 8.51x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
24 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 20892 contig of 20892 bp in length
20993 39343 contig of 18351 bp in length
39444 52928 contig of 13485 bp in length
53029 62642 contig of 9624 bp in length
62743 75229 contig of 9479 bp in length
72321 82201 contig of 9881 bp in length
82302 89905 contig of 100 bp
90006 97086 contig of 7081 bp in length
97187 97186 gap of 100 bp
97187 104116 contig of 6930 bp in length
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125394 125493: gap of 100 bp
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Location/Qualifiers
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Sequence updated (26-May-2000)
 NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence is arbitrary. Gaps between the contigs are represented by runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number be preserved.

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101731	101830: gap of 100 bp
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137207	137207: gap of 100 bp
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Job time : 1982 secs

